

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
26 July 2001 (26.07.2001)

PCT

(10) International Publication Number
WO 01/53524 A2

- (51) International Patent Classification: C12Q 1/68, G01N 33/574, A61K 48/00, 39/00, 39/395, C07H 21/04, C12N 15/63, C07K 14/47
- (21) International Application Number: PCT/GB01/00188
- (22) International Filing Date: 18 January 2001 (18.01.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data: 0000993.6 18 January 2000 (18.01.2000) GB
- (71) Applicant (for all designated States except US): THE NOTTINGHAM TRENT UNIVERSITY [GB/GB]; Clifton Lane, Nottingham NG11 8NS (GB).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): REES, Robert, Charles [GB/GB]; 48 Longford Road, Bradway, Sheffield S17 4LQ (GB). LI, Geng [CN/GB]; 132 Trent Road, Beeston, Nottingham NG9 1LQ (GB). MIAN, Shahid [GB/GB]; 33 Cheyne Walk, Hocknall, Nottingham NG15 7TR (GB).
- (74) Agents: ELSY, David et al.; Withers & Rogers, Goldings House, 2 Hays Lane, London SE1 2HW (GB).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/53524 A2

(54) Title: CANCER ASSOCIATED GENES AND THEIR PRODUCTS

(57) Abstract: The application discloses cancer-associated genes and their products, especially those identifiable by SEREX. The genes and products are used to identify, track and treat cancer. Preferably the cancer is prostate cancer.

CANCER ASSOCIATED GENES AND THEIR PRODUCTS.

The invention relates to isolated nucleic acid sequences which are expressed in cancers, especially prostate cancers, to their protein products and to the use of the nucleic acid and protein products for the identification and treatment of prostate cancers.

The prostate gland is an accessory sex gland in males which is wrapped around the urethra as this tube leaves the bladder. The gland secretes an alkaline fluid during ejaculation. Cancer of the prostate gland is very serious and represents the second leading cause of death from cancer in men.

Two specific proteins are known to be made in very high concentrations in prostate cancer cells. These are prostatic acid phosphatase (PAP) and prostate specific antigen (PSA). These proteins have been characterised and have been used to follow response to therapy. However, it has been difficult to correlate the presence of these two proteins to the presence of cancer.

Accordingly, there is a need to identify new genes and proteins which are associated with the presence of prostate cancer.

The inventors have used a technique known as SEREX (Serological Identification of Antigens by Recombinant Expression Cloning) to identify genes which are over-expressed in prostate cancer tissue. This technique was published by Sahin *et al* (PNAS (USA), 1995, Vol. 92, pages 11810-11813). SEREX uses total RNA isolated from tumour

biopsies from which poly(A)⁺ RNA is then isolated. cDNA is then produced using an oligo (dT) primer. The cDNA fragments produced are then cloned into a suitable expression vector, such as a bacteriophage and cloned into a suitable host, such as E.coli. The clones produced are screened with high-titer IgG antibodies in autologous patient serum, to identify antigens associated with the tumour.

The inventors have used this technique to identify a number of genes and gene products associated with prostate cancer. Furthermore, preliminary results have found that some antigens identified by this technique have been also identified by the inventors as being associated with other cancers, such as stomach cancer and oesophageal cancer.

A first aspect of the invention provides an isolated mammalian nucleic acid molecule selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66. Preferably the isolated nucleic acid molecule encodes a mammalian antigen which is expressed in higher than normal concentrations in cancer cells, compared with normal non-cancerous cells. Preferably the cancer is prostate

cancer. The term "higher than normal concentrations" preferably means that the protein is expressed at a concentration at least 5 times greater in tumour cells than normal cells.

The invention also includes, within its scope, nucleic acid molecules complementary to such isolated mammalian nucleic acid molecules.

The nucleic acid molecules of the invention may be DNA, cDNA or RNA. In RNA molecules "T" (Thymine) residues may be replaced by "U" (Uridine) residues.

Preferably, the isolated mammalian nucleic acid molecule is an isolated human nucleic acid molecule.

The invention further provides nucleic acid molecules comprising at least 15 nucleotides capable of specifically hybridising to a sequence included within the sequence of a nucleic acid molecule according to the first aspect of the invention. The hybridising nucleic acid molecule may either be DNA or RNA. Preferably the molecule is at least 90% homologous to the nucleic acid molecule according to the first aspect of the invention. This may be determined by techniques known in the art.

The term "specifically hybridising" is intended to mean that the nucleic acid molecule can hybridise to nucleic acid molecules according to the invention under conditions of high stringency. Typical conditions for high stringency include $0.1 \times \text{SET}$, 0.1% SDS at 68°C for 20 minutes.

The invention also encompasses variant DNAs and cDNAs which differ from the sequences identified above, but encode the same amino acid sequences as the isolated mammalian nucleic acid molecules, by virtue of redundancy in the genetic code.

	U		C		A		G	
U	UUU } Phe UUC } UUA } Leu UUG }		UCU } Ser UCC } UCA } UCG }		UAU } Tyr UAC } UAA* Stop UAG* Stop		UGU } Cys UGC } UGA* Stop UGG Trp	U C A G
C	CUU } Leu CUC } CUA } CUG }		CCU } Pro CCC } CCA } CCG }		CAU } His CAC } CAA } Gln CAG }		CGU } Arg CGC } CGA } CGG }	U C A G
A	AUU } Ile AUC } AUA } AUG** Met		ACU } Thr ACC } ACA } ACG }		AAU } Asn AAC } AAA } Lys AAG }		AGU } Ser AGC } AGA } Arg AGG }	U C A G
G	GUU } Val GUC } GUA } GUG** }		GCU } Ala GCC } GCA } GCG }		GAU } Asp GAC } GAA } Glu GAG }		GGU } Gly GGC } GGA } GGG }	U C A G

* Chain-terminating, or "nonsense" codons.

** Also used to specify the initiator formyl-Met-tRNA^{Met}. The Val triplet GUG is therefore "ambiguous" in that it codes both valine and methionine.

The genetic code showing mRNA triplets and the amino acids which they code for.

The invention also includes within its scope vectors comprising a nucleic acid according to the invention. Such vectors include bacteriophages, phagemids, cosmids and plasmids. Preferably the vectors comprise suitable regulatory sequences, such as promoters and termination sequences which enable the nucleic acid to be expressed upon insertion into a suitable host. Accordingly, the invention also includes hosts comprising such a vector. Preferably the host is *E.coli*.

A second aspect of the invention provides an isolated protein or peptide obtainable from a nucleic acid sequence according to the invention. As indicated above, the genetic code for translating a nucleic acid sequence into an amino acid sequence is well known.

The invention further provides polypeptide analogues, fragments or derivatives of antigenic polypeptides which differ from naturally-occurring forms in terms of the identity of location of one or more amino acid residues (deletion analogues containing less than all of the residues specified for the protein, substitution analogues wherein one or more residues specified are replaced by other residues in addition analogues wherein one or more amino acid residues are added to a terminal or medial portion of the polypeptides) and which share some or all properties of the naturally-occurring forms. Preferably such polypeptides comprise between 1 and 20, preferably 1 and 10 amino acid deletions or substitutions.

Preferably the protein or peptide is at least 95%, 96%, 97%, 98% or 99% identical to the sequences of the invention. This can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix; Genetics Computer Group, University Research Park, 575 Science Drive,

Madison, WI 53711). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The nucleic acids and proteins/peptides of the invention are preferably identifiable using the SEREX method. However, alternative methods, known in the art, may be used to identify nucleic acids and protein/peptides of the invention. These include differential display PCR (DD-PCR), representational difference analysis (RDA) and suppression subtracted hybridisation (SSH).

All of the nucleic acid molecules according to the invention and the peptides which they encode are detectable by SEREX (discussed below). The technique uses serum antibodies from prostate cancer patients to identify the molecules. It is therefore the case that the gene products identified by SEREX are able to evoke an immune response in a patient and may be considered as antigens suitable for potentiating further immune reactivity if used as a vaccine.

The third aspect of the invention provides the use of nucleic acids or protein/peptides according to the invention, to detect or monitor prostate cancer.

The use of a nucleic acid molecule hybridisable under high stringency conditions, a nucleic acid according to the first aspect of the invention to detect or monitor prostate cancer is also encompassed. Such molecules may be used as probes, e.g. using PCR.

The expression of genes, and detection of their protein products and/or peptides may be used to monitor disease progression during therapy or as a prognostic indicator of the initial disease status of the patient. There are a number of techniques which may be used to detect the presence of a gene, including the use of Northern blot and reverse transcription polymerase chain reaction (RT-PCR) which may be used on tissue or whole blood samples to detect the presence of cancer associated genes. For protein and/or peptide sequences in-situ staining techniques or enzyme linked ELISA assays or radio-immune assays may be used. RT-PCR based techniques would result in the amplification of messenger RNA of the gene of interest (Sambrook, Fritsch and Maniatis, Molecular Cloning, A Laboratory Manual, 2nd Edition). ELISA based assays necessitate the use of antibodies raised against the protein or peptide sequence and may be used for the detection of antigen in tissue or serum samples (McIntyre C.A., Rees R.C. *et. al.*, Europ. J. Cancer 28, 58-631 (1990)). In-situ detection of antigen in tissue sections also rely on the use of antibodies, for example, immuno peroxidase staining or alkaline phosphatase staining (Gaepel, J.R., Rees, R.C. *et.al.*, Brit. J. Cancer 64, 880-883 (1991)) to demonstrate expression. Similarly radio-immune assays may be developed whereby antibody conjugated to a radioactive isotope such as I^{125} is used to detect antigen in the blood (Turkes, A., *et al.*, Prostate-specific antigen - problems in analysis. Europ. J. Cancer. 27, 650-652 (1991)).

Blood or tissue samples may be assayed for elevated concentrations of the nucleic acid molecules, proteins or peptides.

Kits for detecting or monitoring cancer, such as prostate cancer, using polypeptides, nucleic acids or antibodies according to the invention are also provided. Such kits may additionally contain instructions and reagents to carry out the detection or monitoring.

The fourth aspect of the invention provides for the use of nucleic acid molecules according to the first aspect of the invention or protein/peptide molecules according to the second aspect of the invention in the prophylaxis or treatment of cancer, or pharmaceutically effective fragments thereof. By pharmaceutically effective fragment, we mean a fragment of the molecule which still retains the ability to be a prophylactant or to treat cancer. The cancer may be prostate cancer.

The molecules are preferably administered in a pharmaceutically amount. Preferably the dose is between 1 $\mu\text{g/kg}$. to 10 mg/kg .

The nucleic acid molecules may be used to form DNA-based vaccines. From the published literature it is apparent that the development of protein, peptide and DNA based vaccines can promote anti-tumour immune responses. In pre-clinical studies, such vaccines effectively induce a delayed type hypersensitivity response (DTH), cytotoxic T-lymphocyte activity (CTL) effective in causing the destruction (death by lysis or apoptosis) of the cancer cell and the induction of protective or therapeutic immunity. In clinical trials peptide-based vaccines have been shown to promote these immune responses in patients and in some instances cause the regression of secondary malignant disease. Antigens expressed in prostate cancer (or other types of cancers) but not in normal tissue (or only

weakly expressed in normal tissue compared to cancer tissue) will allow us to assess their efficacy in the treatment of cancer by immunotherapy. Protein or peptide derived from the tumour antigen may be administered with or without immunological adjuvant to promote T-cell responses and induce prophylactic and therapeutic immunity. DNA-based vaccines preferably consist of part or all of the genetic sequence of the tumour antigen inserted into an appropriate expression vector which when injected (for example via the intramuscular, subcutaneous or intradermal route) cause the production of protein and subsequently activate the immune system. An alternative approach to therapy is to use antigen presenting cells (for example, dendritic cells, DC's) either mixed with or pulsed with protein or peptides from the tumour antigen, or transfect DC's with the expression plasmid (preferably inserted into a viral vector which would infect cells and deliver the gene into the cell) allowing the expression of protein and the presentation of appropriate peptide sequences to T-lymphocytes.

Accordingly, the invention provides a nucleic acid molecule according to the invention in combination with a pharmaceutically-acceptable carrier.

A further aspect of the invention provides a method of prophylaxis or treatment of prostate cancer comprising the administration to a patient of a nucleic acid molecule according to the invention.

The protein/peptide molecules according to the invention may be used to produce vaccines to vaccinate males against prostate cancer.

Accordingly, the invention provides a protein or peptide according to the invention in combination with a pharmaceutically acceptable carrier.

The invention further provides use of a protein or peptide according to the invention in a prophylaxis or treatment of a cancer such as prostate cancer.

Methods of prophylaxis or treating prostate cancer, by administering a protein or peptide according to the invention to a patient, are also provided.

Vaccines comprising nucleic acid and/or proteins and peptides according to the invention are also provided.

The proteins and peptides of the invention may be used to raise antibodies. In order to produce antibodies to tumour-associated antigens procedures may be used to produce polyclonal antiserum (by injecting protein or peptide material into a suitable host) or monoclonal antibodies (raised using hybridoma technology). In addition PHAGE display antibodies may be produced, this offers an alternative procedure to conventional hybridoma methodology. Having raised antibodies which may be of value in detecting tumour antigen in tissues or cells isolated from tissue or blood, their usefulness as therapeutic reagents could be assessed. Antibodies identified for their specific reactivity with tumour antigen may be conjugated either to drugs or to radioisotopes. Upon injection it is anticipated that these antibodies localise at the site of tumour and promote the death of tumour cells through the release of drugs or the conversion of pro-drug to an active metabolite. Alternatively a lethal effect may be delivered by the use of antibodies conjugated to

radioisotopes. In the detection of secondary/residual disease, antibody tagged with radioisotope could be used, allowing tumour to be localised and monitored during the course of therapy.

The term "antibody" includes intact molecules as well as fragments such as Fa, F(ab')₂ and Fv.

The invention accordingly provides a method of treating prostate cancer by the use of one or more antibodies raised against a protein or peptide of the invention.

The cancer-associated proteins identified may form targets for therapy.

The invention also provides nucleic acid probes capable of binding sequences of the invention under high stringency conditions. These may have sequences complementary to the sequences of the invention and may be used to detect mutations identified by the inventors. Such probes may be labelled by techniques known in the art, e.g. with radioactive or fluorescent labels.

The invention will now be described by reference to the following figure and examples:

Figure 1 shows RT-PCR of different tumour samples showing over-expression of MTA-1 (SEQ.ID.57).

Technique used to identify genes encoding tumour antigens (SEREX technique)

The technique for the expression of cDNA libraries from human prostate cancer tissue is described, and was performed according to published methodology (Sahin et.al. Proc Natl. Acad. Sci. 92, 11810-11813, 1995).

SEREX has been used to analyze gene expression in tumour tissues from human melanoma, renal cell cancer, astrocytoma, oesophageal squamous cell carcinoma, colon cancer, lung cancer and Hodgkin's disease. Sequence analysis revealed that several different antigens, including HOM-MEL-40, HOM-HD-397, HOM-RCC-1.14, NY-ESO-1, NY-LU-12, NY-CO-13 and MAGE genes, were expressed in these malignancies, demonstrating that several human tumour types express multiple antigens capable of eliciting an immune response in the autologous host. This represents an alternative and more efficient approach to identify tumour markers, and offers distinct advantages over previously used techniques:

- 1) the use of fresh tumour specimens to produce the cDNA libraries obviates the need to culture tumour cells *in vitro* and therefore circumvents artefacts, such as loss or neo-antigen expression and genetic and phenotypic diversity generated by extended culture;
- 2) the analysis is restricted to antigen-encoding genes expressed by the tumour *in vivo*;
- 3) using cDNA expression cloning, the serological analysis (in contrast to autologous typing) is not restricted to cell surface antigens, but covers a more extensive repertoire of cancer-associated proteins (cytosolic, nuclear, membrane, etc.);
- 4) in contrast to techniques using monoclonal antibodies, SEREX uses poly-specific sera to scrutinise single antigens that are highly enriched in lytic

bacterial plaques allowing the efficient molecular identification of antigens following sequencing of the cDNA. Subsequently the tissue-expression spectrum of the antigen can be determined by the analysis of the mRNA expression patterns using northern blotting and reverse transcription-PCR (RT-PCR), on fresh normal and malignant (autologous and allogeneic) tissues. Likewise, the prevalence of antibody in cohorts of cancer patients and normal controls can be determined.

Construction of cDNA expression libraries, screening and sequencing

The detailed methodology for SEREX expression cloning established by the inventors is as follows: Total RNA is isolated from fresh prostate cancer tissues using the guanidium thiocyanate-phenol-chloroform extraction method; RNA integrity is determined by electrophoresis in formalin/MOPS gels. Poly(A)+ RNA is prepared by applying the prepared RNA sample to a column of oligo (dT) cellulose and cDNA expression libraries is constructed from 5-8 μ g of poly(A)+ RNA; first-strand synthesis is performed using an oligo(dT) primer with an internal *Xho* I site and 5-methyl-CTP. cDNA is ligated to *Eco*RI adaptors and digested with *Xho* I and cDNA fragments are cloned directionally into the bacteriophage expression vector, packaged into phage particles, and used to transfect *Escherichia coli*. Immuno-screening for the detection of clones reactive with antibodies present in diluted autologous serum is then performed. Transfection for primary screening and plaque transfer onto nitrocellulose membranes is followed by pre-incubation of the membranes with an alkaline phosphatase-conjugated antibody specific for human IgG. Reactive clones representing expressed IgG heavy chains visualized by staining are eliminated from the study. These pre-stained membranes are then incubated with the autologous patient serum, and binding to recombinant proteins expressed in lytic plaques

detected by incubation with an alkaline phosphatase-conjugated goat anti-human IgG, and differentiated from the IgG-heavy chain transcripts. The reactive clones are sub-cloned, purified, and *in vitro* excised to pBK-CMV plasmid forms. Plasmid DNA is prepared using the Wizard (Trade Mark) Miniprep DNA purification system (Promega Corp., Southampton, UK). The inserted DNA is evaluated by restriction mapping, and clones representing different cDNA inserts sequenced using the automated sequencer.

Expression of Antigens in Different Cancers

The expression of metastasis associated 1 (MTA1) (SEQ.ID.57) in cancer samples was compared with that in corresponding normal tissues by semi-quantitative reverse-transcription polymerase chain reaction (RT-PCR). RT-PCR was carried out using processes well known in the literature. A relative over-expression of MTA1 mRNA (normal/tumour ratio ≥ 2) was observed in esophageal cancer (3/7) and head and neck tumour (1/7) (Table 1). See Figure 1, tracks 6 and 8. Testis did not show any over-expression. GAPDH (Glyceraldehyde-3-phosphate Dehydrogenase) expression was also tested as a control. No difference in expression was normal tissue and observed between tumours.

Table 1

Tumour type	Positive rate
Esophageal cancer	3/7
Head and neck tumour	1/7

Table 2 shows the results of further studies of a variety of sequences in different tumours. " - " indicates not studied. This table shows that the proteins are immunogenic in a higher portion of patients with cancer than controls since the patients have antibodies against the cloned protein product.

Table 2

Serological responses in cancer patients and controls to the protein products of genes cloned from the DNA library using SEREX.

SEQ ID #	Gene size bp	Identity	Immunoscreening with sera from :					Co Ca	Ga Ca
			Controls	BPH	Prostate Ca	Head & Neck Ca			
8	Pr III-41 3500 137,144	Unknown	0/7	-	4/10	2/4	-	-	
10	Pr III-90 3000 102,108	Unknown	0/10	0/2	2/7	2/4	-	-	
12	Pr III-104 1500	Unknown	0/8	0/2	2/7	2/4	-	-	
16	Pr III-133 1550	Unknown	0/5	0/2	4/7	-	-	-	
18	Pr III-147 1100	Unknown	1/10	0/2	8/12	2/4	0/2	-	
50	Pr III-157 400	Hu Ribosomal Protein S10	0/4	-	5/10	1/4	-	-	
57	Pr III-176 2600	MTA1	0/13	0/3	2/13	-	0/2	0/2	
60	Pr III-197 1200	ALG2	1/17	0/3	4/13	3/4	0/2	0/2	
29	Pr III-213 2500	Unknown	0/6	0/2	4/12	2/4	0/2	-	

Serum samples from:

Controls
BPH- Benign Prostatic Hyperplasia
Prostate Cancer
Head and Neck Cancers
Co Ca-Colon Cancer
Ga Ca-Gastric Cancer

Table 3 shows some of the mutations identified by the inventors.

Table 3

SEQ ID #	Gene	Identity	Mutation
35	PrIII-30	Human geminin.	Point mutation at nt 78 (A to C)
34	PrIII-13	Human glutamyl-prolyl-tRNA synthetase	261 nt longer at 5' of mRNA. There is a starting code (ATG) in this region. This clone may be a new isoform.
43	PrIII-118	Human poly(ADP-ribose) polymerase mRNA.	Point mutation at nt 79 (C to G) and nt 145 (G to A).
44	PrIII-119	Human tankyrase	Point mutation at nt 2410 (G to A).
52	PrIII-163	Human mitochondrial DNA	Point mutation at nt 10769 (A to G).
60	PrIII-197	Human calcium binding protein (ALG-2) mRNA.	6 nt deletion from nt 487 to 492 (GGTTTC).
65	PrIII-219	Human FACLS for fatty acid coenzyme A ligase 5	Point mutation at nt 758 (A to G)
66	PrIII-224	Human DNA-binding protein (HRC 1) mRNA	129 nt deletion in exon 2. This clone may be an alternatively spliced isoform.

Mutations detected in the sequence of genes cloned by SEREX.

SEQ ID 1

PR2-7A Human mRNA for KIAA0160 gene

GGCGGGTCCGGGGCCACGCGCGGGGTCCGGGGGAGGCGGCTTCGGGGGTCGGCGGCGGT
GGCGGGCGGCGACGGCTTCGGGCGGCAATCCGGCGCGGAGCTGTGGAGGGGGTGGA
GTTACTCGGCCTCCTCCTCCTCCTCGCGCGGCGGACGCGGGGGCTGCGGTGTACCGGT
GAAGAAGCCGAAATGGAGCACGTCCAGGCTGACCACGAGCTTTCTCCAGGCGCTTGA
AAGCCCAACACAGATCTATAGATTCTTCGAACCTCGGAATCTCATGACCCAAATATTTTG
CACAAGAACTCTACTTACATGTCTCATCGAACTCCAGAACAAACATCAAAGGGAACAA
TTTAAAGTTGATGATATGTTATCAAAGTAGAGAAAATGAAAGGAGAGCAAGAA

SEQ ID 2

PR2-1A Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA

ACAGGTGAAAAACCAATACTTTCTAGGGATGACCTTGATGACATAATTCACTGATCTCA
AACAGCTCAGAGGACGGTGACTCGCTTGTCTGTAATTGTAAGAAATCATATTACTCATT
GATCAACATGAAATGAAGTGTAAGAGATTGTGTTCACCTATTGAAAAATTAAGGCACTTT
GTTTATGTGAAAAAGTTAAACAGAACTTAAAGATAATCACTGTGAGCAACTTAGAGTAAAAA
TTGAAAACTGAAATAAAGGCTAGTGTACTACAAAAGAGACTATCTGAAAAAGAGAA
ATAAAATCGCAATTAAGCATGAAACACTTGAATTGAAAAAGAACTCTGTAGTTTGAGA
TTTGGCTACAGCAAGAAAAAAGAAAAAGAAAGAAATGTTGA

SEQ ID 3

PR2-21 2 Human JK-recombination signal binding protein (RBPJK) gene

GAGAGTTTGTGGAAGATGGCGCCTGTTGTGACAGGAAAAATTTGGTGAGCGGCCTCCACCT
AAACGCACTTACTAGGGAAGCTATGCGAAATTATTTAAAGAGCGAGGGGATCAACACAGT
ACTTATTCTTCATGCAAAAGTTGCACAGAACTCATATTGGAATGAAAAAGGTTTTTTTTGC
CCACCTCCTTGTGTATATCTTATGGGCAGTGGAATGGAAGAAAAAAGAAACAAATGGAA
CGCGATGGTGTGTTCTGAAACAAGAGTCTCAACCGTGTGCATTATTGGGATAGGAAATAGT
GACCAAGAAATGCAGCAGCTAAACTTGGAGGAAAGACTATTGCACAGCCAAACATTG
TATATATCTGACTA

SEQ ID 4

PR2-5A Human mRNA for E6-AP isoform-I

GATTCCGGAAGATGATGGAGACATTTTCAGCAACTTATTACTTATAAAGTCATAAGCAATGA
ATTTAACAGTCGAAATCTAGTGAATGATGATGATGCCATTGTTGCTGCTCGAAGTGCTTG
AAAATGGTTTACTATGCAAAATGTAGTGGGAGGGGAAAGTGGACACAAATCACAATGAAGA
AGATGATGAAGAGCCCATCCCTGAGTCCAGCGAGCTGACACTTCAGGGAACCTTTGGGGAG
AAGAAAGAAAGAAACAAGAAAGGTTCTCGAGTGGACCCCTGGAAACTGAACTTGGTGTGTT
AAAACCTGGATTGTGCAAAACCACTTATCCCTTTGAAGAGTTTATTAATGAACCACCTGA
ATGAGGTTCTAGAAATGGATAAGATTACTTTT

SEQ ID 5

PR2-20 3 Human mRNA for TPRD

GGAATAATGTCTTACCCCTGACTGTGAAGGTGTCATTCTTAAGATTATCATCTTCAGCAGTG
GTGGTGAAGTTAAATGTGAATTTGAACACAAAGGTCATAAAGAAAAAGGTTCTCCCAAGAC
CTATTCTGAAACAGAAATGTTCTAGCCTAGAGAAACTAAGACTGAAAGAAAGACAAAAAAT
TGAAGGAAAGAGATCCAAAAAAGAAAGCAAAAAAGTTAGCAAGAAAGAAATGGAGGA
GGACTTAAGAGAAAGTAATCCACCCAAAAATGAAGACAGAAAGAACTGTAGACAAATGT
TCAAGCGTTGTGAGTTCTGTATGACAGAAATCTACAGTGTATAAAGCAGTATGCTTGACA
GGATTAATCCGGCATACAGAAATACAGCCATGCTTCTAAAGAATTGTTT

SEQ ID 6

PR2-1B Unknown

GGGAAGCAGAAAGGATTGGAGTTCCTTTTAAAGTGATTCCTTCCTTCCCTTTTCACTTTT
CCACTGTGGGTGTTATTATCCTGACAATTTGTGCATACATTTCTGTCTTTAAAAAATAACTG
TATACTAAGCAAACTCAGGTCTTAAAAATAAATATGAATTTAGATTCCATACGATTA
ATTGAGAAACACAGACTCTCCAGATGCAACAATCATCAATTAAGTCAACGCGCGACATG
GTGGCCCTGCTCACCCCCAGGGATACCTGTAATACCTGCTTCCCACCTTCATGGGCTAC
AATCTCATGCTGTCAAAATTTCTGTGCTCACTCATATAACACCACAAATGGGATATTTGTG

AAGAACTTCGCTGCGGAGCT

SEQ ID 7

Pr2-2 Unknown

AGGGACAGCTCTTGCA TCGAGACCCCTTCACTGTCATCTGTGGCCGAAAGAAGTGCCTTCG
CCATGTCTTTCTCTTCGAGCATCTCCTCTGTTCAGCAAGCTCAAGGGCCCTGAAGGGGGG
TCAGAGATGTTTGTTTACAAGCAGGCCCTTAAAGACTGCTGATATGGGGCTGACAGAAAC
ATCGGGGACAGCGGACTCTGCTTTGAGTTGTGTTTCGGCGCGCGCGCTGCACGAGAGGCA
TACACTCTGCAGGCAACCTCACCAGAGATCAAATCAAGTGGACAAGTTCTATTGCCAG
CTGCTGTGAGACAGGCAAGCCCAACAAGGAGCTCCGAGTGCAAGCAGATGGTGTCTATG
GCATTGGGAATAAACCTTCTGGACATAAAGCCCTTGGGGAGCGA

SEQ ID 8

Pr3-41 Unknown

GCGGCGGCGGCCCTCGCAGCAGCTGGCGGCGGGCCCCCAGCA
GTTTCGCGCTCTCCAACCTCCGCGGCCATCCGGGCGGAGATCCAGCGCT
TCGAGTCCGTGCATCCCAATATCTACGCCATCTACGACCTGATCGAGC
GCATCGAGGATTTGGCGCTGCAGAACAGATCCGGGAGCAGCTCATC
TCATCGAGGACTCGTTTGTGAACAGCCAGGAGTTGACGCTGACGCC
CTCCGTACCGGAGCTTAAAGTGGGCATAGTGGGGAACCTGTCTAGCG
GGAAGTCAAGCCCTGGTGACCCGCTATCTGACGGGACCTATGTCCA
GGAAGGAGTCCCTGAAGGGGGCGGTTTAAAGAGGAGATTGTGGTG
GATGGCAGAGTTCTGCTGTGATC

SEQ ID 9

Pr3-42 Unknown

GGCTGGCAGTAGAGGTGACCCAGGCGGTGGCGGCGGAGGCGGCACC
GATTGCTGTGTGCGGCCAGTGGCGCGGAAGTCGCGGTAGAGCGTAG
CCCCACGCCCTCCCCCGTCCGCGCCCTCCCTCTTTCCCTGGGGATG
GAGAAGGCGACGGTTCTGTGTGGCGGCGGCGACGGCTTGCAGAAGG
AGAAGGGAGCCCCCGCGGTGGCGGCTTGTGGCGGGCCCCCGCG
GGCGGCGGAGGTCGGCGGCGGCGTTGGCGGCAGCAGCAGAGCTCGC
TCGGCCTCGTCTCCTCGTGGGATGGTGCGAGTCTGCGACCTGCTCT
GAAGAAGAAGCCCGCAGCAGCAGCACCACAAGGCCAAGCGTAAC
CGGACTTGCCACCCCCAGCAGCAGCGAAAC

SEQ ID 10

Pr3-90 Unknown

GCGGCGGCGGCCCTCGCAGCAGCTGGCGGCGGGCCCCCAGCA
GTTTCGCGCTCTCCAACCTCCGCGGCCATCCGGGCGGAGATCCAGCGCT
TCGAGTCCGTGCATCCCAATATCTACGCCATCTACGACCTGATCGAGC
GCATCGAGGATTTGGCGCTGCAGAACAGATCCGGGAGCAGCTCATC
TCATCGAGGACTCGTTTGTGAACAGCCAGGAGTTGACGCTTGAAGC
GCTCCGTACCGGAGCTTAAAGTGGGCATAGTGGGGAACCTGTCTAGC
GGGAAGTCAGCCCTGGTGACCCGCTATCTGACGGGGACCTATGTCCA
GGAGGAGTCCCTGAAGGGGGCGGTTAAGAAGGAGATTGTGGTGGA
TGGCAGAGTTCCTGCTGC

SEQ ID 11

Pr3-93 Unknown

ATTATGAAGTAACTGAACTTTGGTCAAGCATGGTGCCTGTGTAAATG
CAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTCTAAGA
ACAGGGTTGAAGATATGTTCTCTCTTAAGTATGGGTGCAGACCCAA
CACTGCTCAATTGTCAATAAAAGTGCTATAGACTTGGCTCCACAC
CACAGTTAAAGAAAGATTAGCATATGAATTTAAGGCCACTCGTTGC

20

TGCAAGCTGCACGAGAAGCTGATGTTACTCGAATCAAAAAACATCTCT
CTCTGGAAATGGTGAAATTTCAAGCATCCTCAAACACATGAAACAGCAT
TGCATTGTGCTGCTGCATCTCCATATCCCAAAGAAAGCAAAATATGTG
AAGTGTGCTAGAAAAAGC

SEQ ID 12

Pr3-104 Unknown

CCTCAGCATACCCACCGAGCAGCTGCCAGCCTGGGGCTGAGGGTGGGC
ATGAGGCAGGAGTCAGCACTTGGACCTAGGGATGTGAGGTTTTCTGT
GCCCAAGTTTGTGGGAAGGTGGGCACTACTGCTGGGCCACAGACA
CAGCCA GCTGGCAAAGGGAGGCTAGCCCAGCAGAGAGATGAGGA
CATTTTGTCTTCTCTTCATGCCACAGCATGAGCTGAGCTTCTGCTTT
GCTGGAAATGAAATAAACTTGGTATGAATTGTGCCAAGGCCCTCCCA
GTTGTATCCTCGCTCTTGTGTGCCCTCCCTTGTCTTGCCTCCCAACC
CACACCCATGCCCTGTTTCTTACAGATTTTGATATTGTCTAATGTG
TAATAGAACCAGCCGAGTCCCA

SEQ ID 13

Pr3-113 Unknown

CTTACCTCATTCTGAATGTGCATTTCCAGCCTTCTGTCTCAGAGC
TATTGTTCAAGCAGAAAAAAGCTGCTTTTATTACA

SEQ ID 14

Pr3-122 Unknown

GAGAGAACTAGTCTCGAGTTTTTTTTTATTCTTCTATATTCTATGAAT
ATGGTGCTGCTCCTGTCATTTAATTATTATAATATATGTGAAGTCTGG
AGGTAAA

SEQ ID 15

Pr3-124 Unknown

TCGATCCTTAGTGACTTAACAATCAGGCCTTAATTGAAACACACACAC
ACATTGTTATTGACAGTGTAGAAATCTGACTCATAGAAAAATTCAACC
CATATTTAGTTAGCAGACTAACAGGAACAGCAGCAGCAGCAGCAGCT
GGTCATGCTTCTGTGTGTGCTAGCAACAAGAAACCATGACAGCAAG
GCCCAAAACAGGAACCTCCTGCATTTTCTCATCTGTGATGAGGCACAC
TTGATGCTGGGGATTAATGAGCCTGAAGATATAAAGCAGTGTTTACC
ACTGGAAATGTCTCTACACTAAAAGCAGAGGTAAAGTATCAATGCA
AACCAGTGCAGCTATAAAGCCTTGATTTTCTCGGAAATTATGTACAA
ACTAATACAAAATATCTCATTACTTGAAAC

SEQ ID 16

Pr3-133 Unknown

GCTACGGCTGCTCCGGAGCTGGTGGCGCCGCGATAGGAGAGCCGAT
GGCCAAGTGGGGTGAGGGAGACCCACGCTGGATCGTGGAGGAGCGG
GCGGACGCCACCAACGTCACAACTGGCACTGGACGGAGAGAGATGC
TTCAAATTGGTCCACGGATAAGCTGAAACACTGTTCTTGGCAGTGCA
GGTTCAAAATGAAGAAGTCAAGTGTGAGGTGACGGAAAGTGAGTAAGC
TTGATGGAGAGTCAATCCATTAA CAATCGCAAAGGGAACTTATCTTCT
TTTATGAATGGAGCGTCAAACCTAAACTGGACAGGTACTTCTAAGTCAG
GAGTACAGTACAAAGGACATGAGGAGATCCCCAATTGTCTGATGAA
AAC

SEQ ID 17

Pr3-140 Unknown

CATTACCTTACAGTGTAACAGGAGTCTAATTTGTATCAATACTATGT
TTTGGTTGTAATATTCAATTCACTACCCCAATGTACAACCAATGAAAT
AAAAGAAGCATTTAAAGGAA

SEQ ID 18

Pr3-147 Unknown

GGCGTGTGGGTCTCGCAGCGTTGCTCACAGAACAGAGTAGAGGCGGC
GGCGGCGGCGGCCGGACCCAGACTGGTAGTGAGGCGTTGGACCCCG
AGCGCGTGCAATGCCGCTGGAGCTGGAGCTGTGTCCCGGGCGCTGG
GTGGGCGGGGACAACCCGTGCTTCATCATTGNCGAGATCGGCCAGAA
CCACAGGCGCGACCTGGACGTAGCCAAAGCGCATGATCCGCATGGCCA
AGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGTCAAGAA
TTCAAGTTTAATCGGAAAGCCTTGGACAGGCCATACACCTCGAAGCA
TTCCTGGGGGAAGACGTACGGGGAGCACAAACGCACATCTGGAGTTCA
GCCATGACCAGTCAGGGAGCTGAGAGGTCC

SEQ ID 19

Pr3-148 Unknown

GACGGACCGAGACCGGAGATGTTTCAAGCCCGGCTCCGGCGGCTTT
ACAGGCGGCTGCAGCGGCGACGAAGACAACGACAGCGACGGCTACG
CCGAAGCACTCGAACCGGGGGTGAAGCCTCCTGCGCCGGCCTTGCT
CGGATCCAGGATGAGAAGACTGATAAAGAAGAAGCTAGCTGAACAG
CTGTAAAAATGCCAAATCTGGGTTCAAAAAACCAATTCAGAGTGAAAA
TTCTGACAGTGACAGCAATATGGTAGAGAAACCATATGGAAGAAAA
GTAAAGACAAGATGTCATCTACAGCAAACTCCAAAAATTGAACGA
AGTGATGTGAGCAAGGAGATGAAGAGAAATCATCCATGAACCGTA
AACTTCCTTTC

SEQ ID 20

Pr3-162 Unknown

GCAGGAGGGGCTTGCCAGCTTCCGCCCGCGCTCGTTTCAGGACCCGGACGGCGGA
TTCGGCGTGCCTCCGCCCGCGCGGGCAGCCGGGGCAGGGAGGCCAGCGAGGGGC
GGCGGTGGCGCGGCCATGGGACTGCGCCGGATCCGGTGACAGCAGGAGCCAACGC
CGCGGGCCTGAGCGCTCTTCTCCGGGGGGCCTCGCCCTCTGTCTCGGGGGCCGG
GGCTCCTGCTCCGGTTGCTGGCGCTGTGCTGGCTGTGGCGGCGGCCAGGATCATGT
CGGGTCCGCGCTGCGCCGGCGGGGGAGCGGCTGCGCGAGCGCCGGCGGAGGCCGT
GGAGCCGGCCGCGAAGCTGTTTCGAGGCGTGCCGAACGGGAGCTGGAACGAGTAAG
AGGCTG

SEQ ID 21

Pr3-180 Unknown

GCCAACTCAGTCCAGCAGAAACAAATGTAGCTGCCATTCTTGGAGTC
TCTGAAAGCTTTATTGGGAAGAAAGCATCAGGCCAAGCCATCGGAAA
GAAGGTGGACAAGAACGTTGTCAACAGGCTATATCTGTCTTTTGTCT
TTATACCTTGCTCAAAGAGACCAACATTTGGACTGTATCTGAAAAAT
TAATATGCCTCGAGGATATATACAAATCTTCTACTGGAACTGCCTC
ATTCTCATCTTGTGTGTACATTTCTGTGAGGAGCTTGAGGGAGTTTT
GGGTTTACAGAGCCCTTTTGGTAGAAGCTTACCAAGAAGCTGACTACT
GTGTAAGGGGACAGAAATTAATCCCTCTATGGGAAGTTCTNGGAGTTTTA
GAGGGTCGAGCAAAACAGTTTTTCAGNGCCNGGTACCAAAAGTCTAA
TGCCTTAGCTAAGCAAAACCTGAANGNTTCTANGNGNCAATTTGTCNTT
TTTTAAGACCCCAAGCCAGCAAATTTTATNCAAAAAATCTNTCNTN
AAAACCAACCTCAAAANGNNAAAAGTCCNAAATGCTTTTNTTCCCG
GGGGGGGGGTTTTCCTCGCAACNGAANTTTTNGNGGGAANTTTT
TTTTAATTTTTTTNG

SEQ ID 22

Pr3-180 unknown

GGGAGGCGGGCGGACGCTTAAGTGAGAAAGGAAAAAAGACAACGAGGAAAAAGGAGG
TGTCCGGGTAGGGCAACGCGCGACACCCGAGGCGCTGGTGGTGGCGCGGATCGAGA
TATTCAGGCTGAAGCAGCTACGGAACGGCAGCGCGCGCGGTGCGACAACTGACTG

22

ACCGAGCCGGGTGGTGGCGGGAGCAGCGGGAGCAGCCGGAACGATGCCGGCCGTGAG
CCTCCGCCCAAGGAGAATGCGCTCTTCAAGCGGATCTTGAGGTGTTATGAACATAA
ACAGTATAGAAATGGATTGAAATCTGTAAACAAATACITTTCTAATCCCAAAATTTGC
AGAGCATGGAGAAACCTTGGCTATGAAAGGATTAACATTGAACTGTTTGGGGAAAA
GGAAGAAGCTTATGAATTGGTTCTAGAGGTTTGAGAAATGACTTGAAGAGTCAATGTG
TGTTGGCCAGCTTTATGGCCTTTTTCAAGGTCANACAAAGAGTNGATGAANNCTT
AANTGTTACAGAAATGGCTAAATGGGATAAGACATCTTAAATTTTAAGGNCCTTCT
TCTACAANTCAATCCAACTNGNGNTCCNGGAACCAAGGTTTANANTTCTTCANTTN
CNCCTCCCAAAGCATTATGNT

SEQ ID 23

Pr3-194 Unknown

CGGTGGCGCGGAGGCGGCACCGATTGCTGTGTCGGCCCCAGTGCGGCCGAAGTGCG
GGTAGAGCGTAGCCCCACGCCCTCCCCCGTCGCGGCCCTCCCTCTTTCCCTGGGGA
TGGAGAAGGCGACGGTTCGGTGGCGGGCGACGGCTGCAGAAGGAGAAGGGAGCC
CCCCGGCGGTGGCGGCTGTGGCGGGCCCCCGCGGGCGGAGGTCGGCGCGCGGT
TTGGCGGACGACGAGAGCTCGCTCGGCCTCGTCTCGTGGGATGGTGGCAGTCT
GGACCTGCTCTGAAGAAAGAGCGCGCAGCAGCAGCAACCAAGGCCAAGCGTA
ACCGGACTTCCGACCCCCACGAGCAGCGAAAGCAGCAGCGACAGCGACAACAGCG
GCGGCGGTGGAGCGCGGTGGAGCGGAAGTGGCGGGCGCGCACCAGCANTAACAA
CAGCGAGGAAANAAAGGACACACACAGGAANAGAGGTTNTGAGGGGAGTTTATTT
GNTCAGATTATTGGAAANTCAANCTTGNAACTTCCAGGTNNCTATAANGTCNN
TGTNGGCATACNTANGAANTANNCCAAANNAAGNTTNTATGGGAGTTTACNAAAC
NCAGTTTGGATC

SEQ ID 24

Pr3-199 Unknown

CTNNGTTTTTTTTTTTTTTTTTCCAGACTCTTCTGTTCTTTATATCTCAGAAAG
GATTGGGTTTTTCAGGTTGCAAATCTTTCCAGCTCTGCATAGGTAGCATCTC
ACTGAGGAATGGAGTATTTACCACCTATTGTTCTGTNCCAGTCTAGTAGAGCTTTAG
CAAAANCTACAGGCAACAAATCTATTTTTAACATCCTGTTACACAAACAAATATGC
TGAGTATGCACACAAATAAATGGTGAAAGAGGCNAAAGAGTGAAAACAATCGTGC
ATGGTAGGAATATTGAATTGNTTACATGTCTCTTAATATTGNTTTAACAGTNATA
TTTTTACATTTTCAATTGGAATGAAAAGCATGTCTGTGTTGCAATAATTTTTCATCG
NNCNCCTATTTTTGATTCCCNANCTAATGAGNAGAAANCAAGTGAATTGCAAAA
TGTTTCCNCCTNAAGGAATNCNCGTNNGAATTTCTGCAGNCTCTGGAGANCTCCN
TANTTANGNCNTATAGGTANNGATCTATACTCCCTCGGGGGTCTTAGCCNTNC
GNNCCTNCCTTCNTCTACNANCAATGTTNTCTANNGCNCTCANNTAANTNCTN
CAGGCCNCAANTGNNTATNNANCCNCCNNTNTC

SEQ ID 25

Pr3-201 Unknown

CCCGGAACCTGCAAGGCCTGGTCTGGGACCCACACAACCGTAGGAGA
CAGGTCTGAATACCCGGGCCAAGAGCCCAAGCTGTGCTGGCCCTCA
GGGTTTCTCTGGAGTCAACGAGCCGTGGTCCACTTCGTGCTGCTG
TGAAGATCCACAGGCACGCTGGGTACAGCAATTCATCAAAGACATGGAA
AACCTGTACCGGTACCGGTGACCCACACTTCAACATCGTCACACT
GACTATAGCAGTGAGGACATGGATGTTGAGATGGCACTGAAGAGGTC
CAAGCTCGGGAGCTACCAAGTACGTGAAGCTAAGTGGAACCTTTGAAC
GCTCAGCTGGACTTCAGGCTGGCATAGACCTCGTGAAGGACCCGCAC
AGCATCATCTTCTCTGTGACCTCCACATCACTTCCCACTTGGAGTCA
TNGATGCCATTCCGAACACTTGTGTGGAGGGAAGAAAGGGCTTTTG
CCCCCTGGTGATAAGGTTGNNTTGGGGGCCNCCCCAANGGCTGAGGC
TCGGGAGGGGAAAAGGGTTGGGNNTTGGATTACAAATTTNCTGANAN
GATGGGGGNTAACCAAAAGGANTCCAAANCTGGGNGGGAAAAANG
GNACTTTTNNAGGAATTTCAANGCN

SEQ ID 26

Pr3-202 Unknown

GTGAGATGAATGTTCCCCCTCAATTCTCCTTATTTGCCAAATATTTT
CATTTCTTTTGTGCTATTATAGAAAATAAAACCATGCATCACA

SEQ ID 27

Pr3-205 Unknown

AGGAACCAAGAAGACATGGTCCCTGTCCTCATGGTTCAGACAGGGAGGCAGACATT
AAACAACATAATTATCAGTTATTCAATTA

SEQ ID 28

Pr3-208 Unknown

GCGACTCGGGGACCTGGAGCTGACGCCTAGACACTTGTATTAGCTTT
AATAGAAGAGAAATGGAGGAGCCATAGAATATTAAGGATGAATTCAG
GAAGGCCTGAGACCATGGAAAACTTGCTGCTCTACACTATTTTCA
AAGGAGAGGTTGCTATGGTGACAGACTATGGGGCCTTATCAAAATC
CCAGGCTGTGCGGAAGCAAGGTCTGGTCCATCGAACTCATATGTCACT
CTGTGCGGTGGATAAGCCCTCTGAGATAGTAGATGTTGGAGATAAAG
TGTTGGTGAAGCTTATTGGCCGAGAGATGAAAAATGATAGAATAAAA
GTATCCCTCTCCATGAAGGTTGTCAATCAAGGGGACTGGGAAAGACC
TTGATCCCAACAATGTTATCATTGAGCAAGAAAGAGANGCGGAGGCGCA
TCCTTCCAGGATTACACTGGGCAGNAAGATCACCCCTTGAGGCTTGTCT
TGACCTACCTCAANAAGNGNGGNTGTAAAGGGCCCTTTGCAAAAAA
TGTTTATGCANCNNGGGGAATTAACCTTTTTTTCNITGGGAAAGGAA
AGGAAAGCCAATCCCCANTTTGNAACCTNCCCTCAGGAATCTTTTAA
NAAAGAGGGGAAAAAANAACCN

SEQ ID 29

Pr3-213 Unknown

CTGTCAATGGCTGCTCCTGTACGTAGTCACGGTCTTGTGCTCTAAGGAA
AACGACAGCAGCTGTTCTTTTTCTACTAGTAGAAGTGACGTTGGTTTCA
TGTTGACAACCTTTGAAGCCATTTGGAAGTGTTTCAGTGGAGAACAAAA
TGAATAACAAGCGGGCTCCTTTTTCTGGAACCTTAGACAATTCAGTA
CATTAGTTTCAACAAGCAGAACTATGAGGCTATGTTGTTGGGACTTT
GCAAAACCAAAATAGTTCAATCAAACCTGGAACATTTTAAATAACTTTC
ATAACAGAATGCAATCAACTGATATCATTAGATATCTCTTTCAGGATG
CATTCATTTTAAATCAGATGTTGGCTTTCAAACAAAGGGCATAAGCC
TCTACAGCCCTTAGAATTGAAGAC

SEQ ID 30

Pr3-214 Unknown

GTATGGCGGCGTCAAAGGTGAAGCAGGACATGCTCCGCCGGGGGG
CTATGGGCCCATCGACTACAAACGGAACCTTGCCGCGTCGAGGACTGT
CGGCTACAGCATGCTGGCCATAGGGATTGGAACCCGTGATCTACGGG
CAGTGGAGCATAATGAAGTGGAACCGTGAGCGCAGGCGCCTACAAAT
CGAGGACTTCGAGGCTCGCATCGCGCTGTTGCCACTGTTACAGGCAG
AAACCGACCGGAGGACCTTGACAGATGCTTCGGGAGAACCTTGGAGGAG
GAGGCCATCATCATGAAGGACGTGCCCCACTGGAAGGTGGGGAGT
CTGTGTTCCACACAACCGCTGGGTGCCCCCTTTGATCGGGGAGCTG
TACGGCTTGCGCACCAAGAGGAGGCTTTCATGCCAGCC

SEQ ID 31

Pr3-2 Homo sapiens geminin mRNA

GCAGGGCTTTACTGCAGAGCGCGCCGGGCACTCCAGCGACCGTGGG

GATCAGCGTAGGTGAGCTGTGGCCTTTTGGCAGGTGCTGCAGCCATA
GCTACGTGCGTTTCGCTACGAGGATTGAGCGTCTCCACCCATCTTGTG
GCTTCACCATCTACATAATGAATCCAGTAGAAGCAGAACCAAGAAG
AAATCAAAGAGAATATAAAGAATAGTTCTGTCCCAAGAACTCTGTGA
AGATGATTACAGCCTTCTGCATCTGGATCTCTTGTGGAAGAGAAAATG
AGCTGTCCCGAGGCTTGTCCAAAAGGAAACATCGGAATGACCACCTTA
ACATCTACAACCTTCAGCCCTGGGGTTATTGTCCAGAATCTAGTGAA
AATAAAATCTTGAGGAGTACCCAGGA

SEQ ID 32

Pr3-8 Homo sapiens scaffold attachment factor A

GCGAACTCGGTGAAAGGAATTGGCGCCGTTGACACCCAGGCGGATCC
GCTCTGCAGCAGCAACCCATCTCCAGCCGAGCCGAGCCGCGCCG
GGGCGGAGGAGCAGCCGACGACGCGCAACAGTGGCCGAGTGAGCG
GAGCCGAGTTTGAGGCGAGCGCCTAGCGGTGAATCGGGGCCCTACCA
TGAGTTCTCGCCTGTTAATGTAAAAAAGCTGAAGGTGTGGGAGCTG
AAAGAGGAGCTCAAGAAGCGACGCCCTTCTGACAAGGGTCTCAAGGC
CGAGCTCATGGAGCGACTCCAGGCTGCGTGGACGACGAGGAGGCC
GGGGGCCGCCCGCCATGGAGCCGGGAACGGCAGCCTAGACCTGG
GCGGGGATTCCGCTGGGA

SEQ ID 33

Pr3-11 Homo sapiens ribosomal protein L32

CCTACGGAGGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTC
AGACCCCTTGTGAAGCCCAAGATCGTCAAAAAGAGAACCAAGAAGTT
CATCCGGCAACGAGTCAGACCGATATGTCAAAATTAAGCGTAACCTGG
GGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC
CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAACAA
GCACATGCTGCCAGTGGCTTCCGGAAGTTCTCGTCCACAACGTCA
AGGAGCTGGAAGTGTCTGATGTGCAACAAATCTTACTGTGCGGA
GATCGCTNACAATGTTTCTTCAAGACCGCAAGGC

SEQ ID 34

Pr3-13 Homo sapiens glutamyl-prolyl-tRNA synthetase

GTCGGGTACGCGCACACGTTGCATCTTCTCCTTTCGCGGGGTCTCT
CGTAGTTCTGGCACGAGCCAGGCGTACTGACAGGTGGACCAAGCGGAC
TGTTGGAGATGGCGACGCTCTCTGTACCGTGAATTCAGGAGACCC
CCGCTAGGAGCTTTGCTGGCAGTAGAACACGTGAAAGACGATGTCAG
CATTTCCGTTGAAGAAGGGAAAGAGAATATCTTCATGTTTCTGA
TGTGATATTCACAGATGTGAATCTACTTCCGTACTTGGCTAGAGT
TGCAACTACAGCTGGGTTATATGGCTCTAATCTGATGGAACATACTGA
GATTGATCACTGGTTGGAGTC

SEQ ID 35

Pr3-30 Homo sapiens geminin mRNA (mutation at nt 220)

GCGGAGTTAGCAGGGCTTTACTGCAGAGCGCGCGGGCACTCCAGCG
ACCGTGGGGATCAGCGTAGGTAGCTGTGGCCTTTTGGAGGTCGTG
CAGCCATAGCTACGTGCGTTCGCTACGAGGATTGAGCGTCTCCACCC
ATCTCTGTGCTTCAACCTACATAATGAATCCAGTAGAAGCAGA
AACAGAAGAAATCAAAGAGAATATAAAGACTAGTTCTGTCCCAAGA
AGAAGCTGAAGATGATTCAGCCCTCTGCATCTGGAATCTTGTGTGA
AGAGAAAAAGAGCTGTCCGACGAGCTGTCCAAAAGGAAACATCGGA
TGACCACCTTAACATCTACAACCTCCAGCCTGGGGGTTATTGTCCAGA
ATTCTAGTGAATAAATAAATTNNGNNGGAGTCAACCCANGGAGATT
TTGATCTTATGATTAAAGGAAATCCATCTTTTAAATTGAAGGGGAA
NGGGCGAGAAAAACGGAAAGGGGNCCTTNTGAAGCACTTAAGGGA
AAATGAGNAACTTCATAAAGNAAATTGACCAANGGACAAATTGAAA
ATGGCCCGCTGAAAAAGGAAAAATAAGACTGGCNCNNAAGTAGCAAAA

CATGTCCNGGTTTTTG

SEQ ID 36

Pr3-43 Homo sapiens DNA-binding protein (HRC1) mRNA

(5' end of the clone corresponds to the beginning of exon 2 of HRC1)

CAGGCATGTTGTTGGGACTGGCGGCCATGGAGCTGAAGGTGTGGGTG
GATGGCATCCAGCGTGTGGTCTGTGGGGTCTCAGAGCAGACCACTGT
CCAGGAAGTGGTCATCGCACTAGCCCAAGCAATAGGCCAGACTGGCC
GCTTTGTGCTTTGTGCAGCGGCTTCCGGAGAAGGAGCGGCAGTTGCTG
CCACAAGAGTGTCCAGTGGGCGCCAGGCCACCTGCGGACAGTTTGC
CAGCGATGTCCAGTTTGTCTGTAGGCGCACAGGGCCAGCCTAGCTG
GGAGGCCCTCCTCAGACAGCTGTCCACCCCGGAACGCTGCCTAATT
CGTGCCAGCCTCCCTGTAAAGCCACGGGCTTGCCTTGGGCTGTGAG
CCCGCAAAACACTGACCCCGAGCCAGCCC

SEQ ID 37

Pr3-49 Homo sapiens vesicle docking protein p115 mRNA

CGAGATTGGAGGCGGTGGAGCCAGCAGTAGGAGTGTGTAGAAGTGGC
GGATTGGGGGCCAGGCCCTGCGGAGGGCGGGGAAGTTGCTCTTTT
TTTTCCGGAGGGGCCGGTAAACCTGGTGGCTGAACGGCAAGATGAA
TTTCTCCGCGGGGTAATGGGGGGTCAAGTGCAGCCGACCCAGCACA
CAGAAGCCGAGACGATTCAAAAGCTTTGTACAGAGTAGCTTCATCT
ACTTTATTGGATGATCGAAGAAATGCTGTTCGTGCTCTCAAATCATTA
TCTAAGAAATACCGCTTGGAAAGTGGGTATACAAGCTATGGAACATCT
ATTCATGTTTACAAACAGATCGTTTCAATTTGAAATATAGGTATG
TTTGGACACACATATAATNNATATCTAA

SEQ ID 38

Pr3-101 Homo sapiens upstream transcription factor, c-fos interacting (USF2)

ACATGCTGGACCCGGGTCTGGATCCCGCTGCCTCGGCCACCGCTGCT
GCCGCCGCCAGCCACGACAAGGGACCCGAGGCGGAGGAGGGCGTGG
AGCTGCAGGAAGGCGGGGACGGCCAGGAGCGGAGGAGCAGACAGC
GGTGGCCATCACCAAGCGTCCAGCAGGCGGCGTTCCGGCAGCCACAAC
TCCAGTACCAAGTTCGCCACAGAGACAAATGGAGGACAGGTGACATAC
CGCGTAGTCCAGGTGACTGATGGTCAAGTGGACGGCCAGGGCGACAC
AGCTGGCGCCGTACAGCTCGTGTCCACCGCTGCTTCGCGGGGGGGCA
AGCAGGCTGTGACCAAGGTG
GGTGTGC

SEQ ID 39

Pr3-109 Homo sapiens DNA-binding protein (HRC1) mRNA (Type I transcript)

GTCGGGGTGGGGCGTTCCCATGCCGCGCGCGGGGCGCTGGCGTG
CGGGCGCCTCCGCGCGCGCCGGGGAAGGGGCAAGTGTCTCCGAGCC
AGGACAGGCATGTTGTTGGGACTGGCGGCCATGGAGCTGAAGGTGTG
GGTGGATGGCATCCAGCTGTGTGTCNTGTGGGGTCTCAGAGCAGAC
ACCTGCCAGGAAGTGGTCAATCGCACTAGCCCAAGCAATAGGCCAGAC
TGCCCGCTTTGTGCTTGTGACAGCGGCTTCGGGAGAAGGAGCGGCACT
GCTTTGCCACAAGAGTGTCCAAGTGGGCGCCAGGCCACCTGCGGAC
AGTTTGCAGCGATGTCCAGTTTGTCTGAGGCGCACAGGGGCCAGC
CTAGCTGGGAGCGCTTCTAGACAGCTGC

SEQ ID 40

Pr3-111 Homo sapiens proteasome sub-unit HSPC mRNA

GAGTCGCGGCGGAAGGAGCCCGCGCCGCCCGCCCGGCATGAGCTA
GCACCGCGCCATCACCGTCTTCTCGCCGACGGCCACCTCTTCCAAG
TGAAGTACGCGCAGGAGGCGGTCAAGAAGGGCTCGACCGCGGTTGG
TGTTGAGGAAGAGACATTGTTGTTCTTGGTGTGGAGAAGAAGTCAG

TGGCCAAACTGCAGGATGAAAGAACAGTGCAGGAAGATCTGTGCTTTG
 GATGACAAACGTCTGCAATGGCCCTTTGCAGGCCCTCACCGCCGATGCAAG
 GATAGTCATCAACAGGGCCCGGGTGGAGTGCCAGAGCCACCGGCTGA
 CTGTGGAGGACCCGGTCACTGTGGAGTACATACCCGCTACATCGCCA
 GTCTGAAGCAGCGTTATACGCAC

SEQ ID 41

Pr3-112 Homo sapiens trans-Golgi p230 mRNA

GCCGAGGCCAGCCAGTGGCACCCGGAAGAAAGAGACGCGCGCGCGG
 CGACGCCGACACCOCTCAGGACGAGTGTCCGGACTTGCCACAGCCCTC
 AAGGAGGAGACGGCGAGGCCGCGGCCCGCTGTCCCTGGTGTAAAG
 AAGTCGCCGTAGCCGTGCGGCCGGGACTGCCGGGCTCTCGCCCTT
 CAGGTTTTCGTTGACACTCAGGACCGTACGTACGCTTGCGCAATGTTT
 AAGAAATGAAACAAAAGATCAAGCGAGGAGCAGCAGCAGCTCCAGC
 AGGCGCTTGGCTCCTGCTCAGGCGTCTCCCAATTCTTCAACACCAACA
 AGAATGAGGAGCAGGACATCTTCATTTCAGAGCAACTGATGAAGGT
 ACACCCAATAGAGAGTCAGGTGACACACAGTCTTTTGA

SEQ ID 42

Pr3-116 Homo sapiens ribosomal protein S14

CACCCCCATCCCCTCTGACAGCACTCGCAGGAAGGGGGTTCGCGGTG
 GTGCGCGTCTGTGAACAAGATTCCTCAAAATATTTCTGTTAATAAAT
 TGCCTTCATGTA

SEQ ID 43

Pr3-118 Homo sapiens poly (ADP-ribose) polymerase mRNA (The clone is 14 nt longer than the polymerase at 5' end; There is a point mutation at nt 159 of the clone)

GCCGCTCAGGCGCCTGCGGCTGGGTGAGCGCACGCGAGGCGGCGAG
 GCGGACGCGTGTCTAGTCTGTGGCTCGGGCTTCGGAGCTTTGC
 CGGCAGCTAGGGGAGGATGGCGGAGTCTTCGGATAAGCTCTATCGAG
 TCGAGTACGCCAAGAGCGGGCGCGCTCTTGCAAGAAATGCAGCGAG
 AGCATCCCCAAGGACTCGCTCCGGA TGGCCATCATGGTGCAGTCGCC
 CATGTTTGATGGAAAGTCCACACTGGTACCACTTCTCCTGCTTCTG
 GAAGGTGGGCCACTCCATCCGGCACCTGACGTTGAGGTGGATGGGT
 TCTCTGAGCTTCGTTGGGATGATCAAGCAGAAAGTCAAGAAGACAGC
 GGAAGCTGGAGGAGTNCAGG

SEQ ID 44

Pr3-119 Homo sapiens tankyrase, TRF-interacting ankyrin-related polymerase (TNKS) mRNA, and translated products (point mutation at nt 129 of the clone)

TAAAGGAAAGTATGAAATCTGCAAGCTCCTTTTAAACATGGAGCAG
 ATCCAACATAAAAGAACAGAGATGGAATAACACCTTTGGATTTGGTAA
 AAGAGGAGACACAGATATTCAGGACTTACTGAGAGGGGATGTGCT
 TTGTTGGATGCTGCCAAGAAAGGCTGCCTGGCAAGAGTGCAGAAGCT
 CTGTACCCCGAGAGAATATCAACTGCAGAGACACCCAGGGCAGAAATT
 CAACCCCTCTGCACCTGGCAGCAGGCTATAATAACCTGGAAGTAGCT
 GAATATCTTCTAGAGCATGGAGCTGATGTTAATGCCAGGACAGGG
 TGGTTTAATCTCTTCAATAATGCGGCATCTTATGGGCATGTTGACA

SEQ ID 45

Pr3-128 Homo sapiens proteasome sub-unit HSPC mRNA

GAAGAAACAAAAGAAAGCATCATGATGAATAAAATGTCTTTGCTTGTA
 ATTTTAAATTCATATCAATCATGGATGAGTCTCGATGTGTAGGCCCTT
 TCCATTCCATTATTCACTGAGTGTCTACAATAAACTCCGTATT
 TTA

SEQ ID 46

Pr3-146 Human poly(ADP-ribose) polymerase mRNA (point mutation at nt 140 of the clone)

CGCATGNCATTACTGCACTGGGGACGTCACCTGCCTGGACCAAGTGT
ATGGTCAAGACACAGACACCCCAACCGGAAGGAGTGGGTAACCCCAAA
GGAATTCGAGAAATCTCTTACCTCAAGAAATTGAAGGTTAAAAAACA
GGACCGTATATTCCCCCAAGAAACAGCGCCTCCGTGGCGGCCACGC
CTCCGCCCTCCACAGCCTCGGCTCCTGCTGCTGTGAACCTCTCTGCTT
ACGACAGATAAGCCATTATCCAACATGAAGATCTGACTCTCGGGAAG
CTGTCCCGGAACAAGGATGAAGTGAAGGCCATGATTGAGAAACTCGG
GGGGAAGTTGACGGGGACGGCCAACAAGGCTTCCTGTGCATAAGCA
CCAAAAAGGAGGTGAAAAAGATGAATAAGAAGATG

SEQ ID 47

Pr3-152 Homo sapiens ribosomal protein L10

AGAACANGGAGCATGTGATTGAGGCCCTGCGCAGGGCCAAGTTCAGG
TTTCTTGGCCGCCAGAGATCCACATCTCAAAAAGTGGGGCTTCAAC
AAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCT
CATCCAGATGGCTGTGGGGTCAAGTACATCCCCAGTCTGTCGGCCTC
TGGACAAGTGGCGGGCCCTGCACTCATGAGGGCTTCCAATGTGCTGC
CCCCCTCTTAATACTACCAATAAATTTACTTCTGTCCAAAAAAA
AAA

SEQ ID 48

Pr3-154 Homo sapiens clone Xu-3 immunoglobulin heavy chain variable region mRNA

GTCGTGGACCTCCTGCACAAGAACATGAACACCTGTGGTTCTTCCTC
CTCCTGTGGGACGCTCCAGATGGGTCTGTCCAGGTCAGTTACAC
GCAGTGGGCGCAGGACTCTGAAGCCTTCGGAGACCTGTCCCTCA
CCTGCOCNTGTCTATGGTGGGTCTTAAGTGGTTATGGCTGGAGCNT
GGATCCGCCAGCCCCAGGGAAGGGGCTTGGAGTGGATTGGGGAAG
TCGACCATCGTGGCAGCGCCAATTACCACTCGGCCCTCCAGAGTCGA
GTCTCCGTATCATTGGACACGTCCAAGAACCAGGTCTCCCTGAGGCT
GAACCTCAGTGACCGCCCGGACACGGCTTTATNCTGTGCGAGAGG
CCTAATAAAGCAATGGCTCTATTGGGG

SEQ ID 49

Pr3-155 Homo sapiens phospholipase C, gamma 1 mRNA

GCCAGATCACGTGGAGCGGGGCGCCGACAAGATCGAGGGGGCCAT
TGACATTCTGTGAAATTAAGGAGATCCGCCAGGGAAGACCTCACGGG
ACTTTGATCGCTATCAAGAAGACCCAGCTTTCGGCCGGACACAGTCA
CATTGCTTTGTCAATCTCTATGGAATGGAAATTCGCCTGAAAAACGCTG
AGCCTGCAAGCCACATCTGAGGATGAAGTGAACATGTGGATCAAGGG
CTTAACCTTGGCTGATGGAGGATACATTGCAGGCCACCCACCCCTGC
AGATTGAGAGGTTGGCTCCGGAAGCAGTTTACTCAGTGGATCGGAAT
CGTGAGGATCGTATATCAGCCAAGGACCTGAAGAACATGCTGTCCCA
GGTCAACTACCGGTTCCCAACC

SEQ ID 50

Pr3-157 Homo sapiens ribosomal protein S10 mRNA

GTACCTTACCAATGAGGGTATCCAGTATCTCCGTGATTACCTTCATCT
GCCCCCGGAGATTGTGCTGCCACCTACGCCGTAGCCGTCCAGAGA
CTGGCAGGCCTCGGCCTAAAGGCTCTGAGGGGTGAGCGACCTGCGAG
ACTCACAAGAGGGGAAGCTGACAGAGATACCTACAGACGGAAGTGTCT
TGCCACCTGGTGCCGACAAGAAAGCCGAGGCTGGGGCTGGGTGACG
AACCGAATTCAGTTTGAAGCGGAAATTTGGTCTGGACGTGTTCAGC
CACCTCAGTAAATTTGAGAGGAGTCTTTTGCATTGAATAAACTTACA

GCCAAAAAACCTTA

SEQ ID 51

Pr3-160 Homo sapiens poly(ADP-ribose) synthetase mRNA

AATCCGGGACACAGGTTTCGGTGCCCTCTCCCTGCGAGGAATGCTC
GGGTGAGCTGGTCTTCAAGAGCGATGCTATTACTGCACTGGGGAGC
TCACTGCCTGGACCAAGTGTATGGTCAAGACACAGACACCCAAACCG
AAGGAGTGGTAACCCCAAAGGAATTCCTGAGAAATCTCTTACCTCA
AGAAATTGAAGGTAAAAAACAGGACCGTATATCCCCCAAGAAAC
AGCGCTCCGTGGCGGCCACGCCCTCCGCCCTCCACAGCCTCGGCTCC
TGCTGCTGTGAACCTCTCTGCTTCAGCAGATAAGCCATTATCCAACAT
GAAGATCCTGACTCTCGGGAAGCTGTCCCGGAACAAGGATGAAGTGA
AGGCATGATTGAGAACTCGGGGGGAAGTTGACGGGGA

SEQ ID 52

Pr3-163 Homo sapiens mitochondrial DNA (A point mutation at nt 169 of the clone)

AGGCTATGTGTTTTGTACAGGGGGTTGAGAATGAGTGTGAGGCGTATT
ATACATAGCCGCCTAGTTTCAAGAGTACTGCGGCAAGTACTATTGAC
CCAGCGATGGGGGCTTCGACATGGGCTTAGGGAGTCAATAAGTGGAG
TCCGTAAAGAGGTATCTTTACTATAAAGGCTATTGTGTAAGCTAGTCA
TATTAAGTTGTGGCTCAGGAGTTGATAGTTCTTGGGCAGTGAGAGT
GAGTAGTAGAATGTTTGTAGTGGCTAGGGTGTGTGAGTGTAAATTA
AGTGGCATGAGTAGGGGAAGGGAGCCTACTAGGGGTAGAAATAGGA
AGTATGTCTCGCTTCAGGCGTTCTGTGGTTGCCTCATCGGGTGAT
GATAGCCAAGGTGGGGATAAGTGTGGTTCCAAAC

SEQ ID 53

Pr3-165 Homo sapiens ribosomal protein S8

GAGCGATGGGCATCTCTCGGGACAACCTGGCACAAGCGCCGCAAAACC
GGGGGCAAGAGAAAAGCCCTACCAAGAAGCGGAAGTATGAGTTGG
GGCGCCAGCTGCCAACACCAAGATTGGCCCCCGCCGATCCACACA
GTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGA
CGTGGGGAATTTCTCTCGGGGCTCAGAGTGTGTACTCGTAAAAACAA
GGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTA
CCAAGACCTGTGTAAGAAATGCATCGTGCTCATCGACAGCACACCG
TACCGACAGTGGTACGAGTCCACTATGCGCTGCCCTGGGCGCAAG
AAGGGAGCCAAGCTGACT

SEQ ID 54

Pr3-168 Homo sapiens ubiquitin specific protease 8 (USP) mRNA

GGCACATTGGCTAAAGGCTCTTTGGAGAATGTTTGGATTCCAAAGA
CAAAACCCAAAAAGAGCAATGGTGAAAAGAAATGAAAAATGTGAGACCA
AAGAGAAAGGAGCAATCACAGCAAAAGGAACTATACACAATGATGACG
GATAAAAAATCATAGCTTGATTATAATGGATGCTCGAAGAATGCAGGA
TTATCAGGATTCTGTATTTTACATTCTCTAGTGTTCCTGAAGAAGC
CATCAGTCCAGGAGTCACTGCTAGTTGGATTGAAGCACACCTGCCAG
ATGATTCTAAAGACACATGGAAGAAGAGGGGNAATGTGGAGTATTG
TGGGTACTTCTTGACTGGGTTTAAGTCTGCCAAAGATTACACGATT
GGAAACCAACTCTCCCGGAGTTTGAAGATGCACITTTTCAGGGGGGAA
AGTAAAAACTGGTCTCGNCATGAGCCTTTGGNTTTAANGGGGGGT
GAAACTGTCTCTTTTNTNCCCCGTTTCCACAAGCTTANGGGGNTCC
CCACCCCNANAAAAANNGGGNTTCATNGGGTTTNCITTTCCCTTNGGAA
AAAAATCTTTTAAACGGGGNCCACCCCTTTTAAAAAN

SEQ ID 55

Pr3-170 Homo sapiens sgk protein kinase

TACNTGTTTNGCTCGCGCCCTGCAGGTCGACACTAGTGGATCCA
AAG
CAACTCCATTGGCAAGTCCCTGACAGCGTCTCGTCACAGCCAGCG
TCAAAGGAAGCTGCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCA
CGGACTCTTTCTCTGTAACCTGTTAGGGCTTGGTTTTAAAGGATTTT
ATGTGTGTTTCCGAATGTTTAGTTAGCCTTTTGGTGGAGCCGCGAGC
TGACAGGACATCTTACAAGAGAATTGACACATCTCTGGAAGCTTAGCA
TCTTATTGACACTGTTCGCTGGAAGCTTTTTGAAGAGCACATTCCT
CTCAGTGAGCTCATGAGGTTTTCAATTTTATTCTCTCTCCAAACGTGG
TGCTATCTCTGAAACGAGCGTTAAGAGTGCCCGCCTTAGACGGAGCA
NGGAGTTTTCTGTAGAAAAGCGGACGCTGTTCTAAAAAANGTCTCTG
CGAGATCTGTCTGGGCTGGTGATGACNAATATTATGAAAATGTGNCC
TTTNTGAANAATAAGGGTTAGCTTCNAACCTTCTTTCGCAAGGGTTC
AAGTTTTTATTNTCTTGGGAATNCCTGGGGAACCCCGGGGAAGGG
GGGATGCCNGANCAAAGGNTTTGTTTAGCCNNAAGGGGACCTTGCG
GACTNCACGGGGAATTTNTTTGTTT

SEQ ID 56

Pr3-174 Homo sapiens mitochondrial genome

GTCACCAAGACCTACTTCTAACCTCCCTGTTCTTATGAATTGGAACA
GCATACCCCCGATTCCGCTACGACCAACTCATACACCTCCTATGAAA
AACTTCTTACCACCTACCTAGCATTACTTATATGATATGTCTCCATA
CCCATTAACAATCTCCAGCAITCCCCCTCAAACCTAA

SEQ ID 57

Pr3-176 Homo sapiens metastasis associated 1 (MTA1) mRNA

GGGACATCTCCAGCACCTCTATCGCCCTGGCCGACAAGCACGCAACC
CTGTCACTCTGCTATAAGGCCGACCGGGGGCGGACAACGGCGAGG
AAGGGGAAATAGAAGAGGAAATGGAGAATCCGGAATGGTGGACCT
GCCCGAGAAACTAAAGCACAGCTGCGGCATCGGGAGCTGTCTCTCT
CCCGGCAGCTGGAGTCTCTGCCCGCCACGCACATCAGGGGCAAGTGC
AQCCTCACCTGCTCAACGAGACCGAGTCGCTCAAGTCTTACCTGGA
GCGGGAGGATTTCTTCTTCTATTCTCTAGTCTACGACCCACAGCAGAA
GACCTGTCTGGCAGATAAAGGAGAGATTTCGAGTAGGAAACCGGTACC
AGGCAGACATCACCGACTTGTAAAGAAAGGCGAGGAGGATGGCCGA
GACCACTCCAGGTTTGGAGACCCAAAGTGTNGGAGGGGCAACACCCA
CTTACAGACAAGCCAGATGNNCAATCTTGGGNGGNGGGCCGCTTTTG
GGGCACCTTCCACGGGNCCTGGACTGAGANNTTCTTCCACACCCAC
TTGCAAGANNCNCNAATTGCTTCNAAAATANNCCCTTTCCNCCCCT
GGGTCTCTTCAAAAATAATTTACAAATTTACAGGC

SEQ ID 58

Pr3-179 Homo sapiens trans-Golgi p230 mRNA

CCGAGGCCAGCCAGTGGCACCCGGAAGAAAGAGACGCGGCGGCGGC
GACGCGACACCTCTCAGGACGAGTGTCCGGAATGCCCCAGAGCTCA
AGGAGGAGACGCGAGGCGGCCGCCCGCTGTCCCTGGTGTAAAGA
AGTCGCCGTAGCCGTGCGGCGCGGACTCCCGGGCTCTCGCCCTTC
AGGTTTCGTTGACACTCAGGACCGTACGTACGTGCGGCATGTTCAA
GAAACTGAAGCAAAAGATCAGCGAGGAGGACGAGCAGCTCCAGCAG
GAACTGGCTCCTGCTAGGCGTCTTCAATTTCTCAACACCAACAAGA
ATGAGGAGCAGGACATCTTCAATTTACAGAGCAACTTGATGNAAGGTA
CACCAATAGAAGAGTTCAAGGTGGACACACAAGTCTTTTGACAGGA
AAGCTTCAGTTCNNGGTGCCCTCGGGGGAGTCTTTGTTTTNGAAGT
CGATAAGGAATTNTTTCCGGNCTTTTTTAAAGAGTTTTTTGGTGCAA
AATNTTTCAAAAAATCCTGAATGATTGACTGGAGGNTCTGCGGTTTTG
ATCCCCCTTTTTGATGNNNGGTAAAAATGGGGGGGATTTNANACG

NTTAAAAAATGTTTCNGGTTGNAAAAAAGAANAANN

SEQ ID 59

Pr3-186 Homo sapiens Surf-5 and Surf-6 genes

AGAAAAACACAAAAGAAATTCCGGAAGCGAGAAGAGAAGGCTGCTGAG
 CACAAGGCCAAAGTCCCTTGGGGGAGAAAATCTCCAGCAGCCTCTGGGGC
 CAGGAGGCCCTGAGGCGAGCCAAAGAGGAAGCAGCTTGGGCTTCCAGCT
 CAGCAGGGAACCCCTGCAGATGGCTTGGCCAAGCTGAGCCTGAGTCTGTG
 TTTGCTCTGGATGTTCTGCGACAGCGACTGCATGAGAAGATCCAGGA
 GGCCCGGGGCCAGGGCAGTGCCAAGGAGCTGTCCCTGCCGCTTG
 GAGAAAAGGCGCGGAGAAAGCAGGAACGGGACCGGAAGAAGAGGA
 AGCGAAAGGAGCTGCGGGCGAAAGANAAGCCAGGAAGGCTGAGGAG
 GCCACGGAGGCCAGGAGGTGGTGGAGGCAACCCAGAGGGGGCCT
 GCACGGACCCNANGAGCCCCGGCTTGTCTTATTAGGGGGGAGGTG
 AGCGAAACAACCGGCCACAAGGGGCACCAAAAAAAAAAAGCANAGT
 TGAAGGGAACCTCNCCTCNCGGAGAATACCGCANTTTTGAACCTGC
 GCNCCGAAAAACCGTTGANAANTCGCCNATGGGGGAAGCCNGACTG
 GGCAANA

SEQ ID 60

Pr3-197 Homo sapiens calcium binding protein (ALG-2) mRNA (6 nt deletion and a point mutation)

GGTCTCTCGTTCGTCGAGGCGCCTCAGCCAGCGCGTGCCTTGGCC
 CATGGCCGCTACTCTTACCGCCCCGCCCTGGGGCCGGCCCTGGGC
 CTGCTGCAGGCGCGCGCTGCGCGACAGAGCTTCTGTGGAACGTT
 TTCCAGAGGGTCGATAAAGACAGGAGTGGAGTGATATCAGACACCGA
 GCTTCAGCAAGCTCTCTCCAACGGCACGTGGACTCCCTTTAATCCAGT
 GACTGTGAGGTGATCATATCCATGTTTGACCGTGAGAACAAGGCCG
 CGCTGAACTTCAGCGAGTTCAOGGTGTGTGGAAGTACATCACGGAC
 TGGCAGAACGTCTTCCGACGTACGACCGGGACAACTCCGGATGAT
 CGATAAGAACGAGCTGAAGCAGGCCCTCTCAGGCTACCGGCTTNTNT
 GACCAAGTCCAACGACATCCTATTGAAAAAGTTTGACAGGCAGGGACG
 GGGCAAAATCGCTTCAACACTTTATCANGGCTGNATTGTCTGAANAG
 GTGGCGGTNTTTTAAACTTCACCCGGATAGGANGTGTTTAAGGGGTG
 ACNAAAAANCTGCCANGNTTTAAAAANTCGAAGACNCGCCCTTGGGAG
 GGCCCACTNGGAAGGCCAATGTNCCNT

SEQ ID 61

Pr3-200 Mus musculus BS4 peptide mRNA

GCGCAGGGATGGCACAAGAAATATCTTCAAGCAAAATTGACCCAG
 TTTTAAAGGGAAGACAGGATTCAACTTTGGAAACCTCCATATACAGAT
 GAAAAATAAAAAAGTTGGTTTGGCATTAAAGGACCTTGCTAAGCAGTA
 CTCTGACAGACTAGAAATGCTGTGAAAAATGAAGTAGAAAAAGTAAAG
 AAGAAATACGTTGCAAGGCAATTGAGCGTGGAAACAGGAAATGACAAT
 TATAGAAACAACGGGAATTGCTACAATCGAAGGTGTTTTACCACCAAGA
 CTAAAAAAGATAGGAAAAAATTTGTTGGAGACCCGATTGCACATCAC
 TGGCAGAGAAGTGGGTCCAAAAATAGCTGAAACCTTTGGACTTCAAG
 AAAATTATATCAAAATGTGCATAAATAAGAAAGCAACTACACTAGGGAA
 AACCTTGAAGAAAGGGGTGGCTCCAATGTGAAAGCGATGGTGCTT
 GACTAAAAACATCTGAAAGGACGACAGGAACTTCCGTTGGGGGAAGAG
 GCAAAANAGGCCACTCAAGAAACANTCGNGNCAGANGGCTTGAATC
 TGGCAGAGACACNAAGNNGGGGACCAAGAACCCNCTTTAACTTNT
 TACNGNCGGCNATN

SEQ ID 62

Pr3-203 Homo sapiens Pig11 (PIG11 mRNA)

GGCTCTGGCACACAGCTGTGCTCACAAAACTAGGGTGGCTTGGTTA
GAGCTAATTGTAGTGAGGCGCTGCAGGTGAGGGGTGAGGGAGGGGGCT
GCAGGTCAGGTAAGATCTGGAAGACAGACGTACAGCTTGGAGGGCAG
GGGGACTCTAAGGCAAGGAGATTTACAGTTGGGAAGGAGGCAGTGG
CAGAGGGGTGAGGGACAGGGGCCCTTAAGTCCAGCGAGGAAAGCTC
GGTGTGGGCCCGCTCTACGCTCCGTTTGGGGTGACCTGGAACGCCTC
TTCTCCAGGCTCCCTCCAGCCATCAGCAGCCTCTTGTCAAGCTTCTGC
CTCGCCCCAGTCTATCCCCAACCCCAAATCAAGACCACCTTTCTTCAC
GGTCACTATTTATCTTTGGTCCTTTTCTTTTGTGAAGAAACATTCACA
AAAACCAAGTGCCNNNCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNAAAACTCGGGAGTCTTTTAAAGGGGGCGNGGC
CNTNGNNTTCCCGGGGGGGGCCCGNAAAGNCCCCATNCTTTNGG
GGGGGGGTNNATNTGGGCCCGNTTAAACNTNGATNGNACCNCTG
GCT

SEQ ID 63

Pr3-206 Homo sapiens F1F0-type ATP synthase sub-unit d mRNA

GCAGCCAGGGTCCGTTGAAGGATCCCAAAATGGCTGGGCGAAAACTTG
CTCTAAAAACCAATTGACTGGGTAGCTTTTGCAGAGATCATACCCAGAG
ACCAAGAGGCCATTGCTAGTTCCTGAAATCCTGGAATGAGACCCCT
ACCTCCAGGTTGGCTGCTTACCTGAGAATCCACCAGCTATCGACTG
GGCTTACTACAAGGCCAATGTGGCCAAAGGCTGGCTTGGTGGATGACT
TTGAGAAGAAAGTTAATGCGCTGAAGGTTCCCGTGCCAGAGGATAAA
TATACTGCCAGGTGGATGCCGAAGAAAAAGAGATGTGAATCTTG
TGCTAGTGGGGTGTCTCTCTCAAAGGCCAGGATTGTAGAATATGAA
GAAAGAGATGGAGAAGATGAAAGAACTTAATTNCTTTTGATCAGATG
ACCAATTGANGGACTTGAATGAAGCTTTTCCAGAAACCAAATTAGACAA
GAAAAAGTNTCCTATTGGNCTACCANCCATTGGGAATTATAAATGA
GTGCGGAGGAAGTTTGGCCTTGNATACCAATTGGCCTTAAATATTATT
TCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAAACCTCGGGG
CTT

SEQ ID 64

Pr3-209 Homo sapiens ribosomal protein L18a

GCTGTCAAGCAGTTCACGACTCCAAGATCAAGTTCCCGCTGCCCCCA
CCGGGTCCTGCGCCGTCAGCACAAAGCCACGCTTCAACCACCAAGAGGC
CAACACCTTCTTCTAGGTGCAGGGCCCTCGTCCGGGTGTGCCCCAA
ATTAACCTCAGGAACGCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA
AAAAAAAC

SEQ ID 65

Pr3-219 Human FACL5 for fatty acid coenzyme A ligase 5

GTGTGCTGCTTCTCAGATGCCAAGACTATGTATGAGGTTTTCAAAAGAG
GACTCGCTGTGCTGACAATGGGCCCTGCTTGGGATATAGAAAAACCA
AACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGC
AGAGTACCTGGGTTCTGCTCTTGATATAAGGTATATAAATCATCACCC
AGACCAAGTTTGTGCGCATCTTGTCTCAGAATAGGCCAGAGTGGATCA
TCTCCGAATTGGCTTGTACACCGTACTCTATGTTAGCTTGTACCTCT
GTATGACACCTTGGGACCAGAAGCCATCGTACATATTGTCAACAAGG
CTGATATCGCGTGGTGTCTGTGACACCCCAAAAGGCATTGGTG
CTGATAGGGAATGTAAGAAGGCTCACCC

SEQ ID 66

Pr3-224 Homo sapiens DNA-binding protein (HRC1) mRNA (The clone contains alternative exon 1a; it might be a new isoform of HRC1)

CCGGATNGGGTCTCCAGGCTGGCGAGCGCCAGGCCAGACTGGCCG
CTTTGTGCTTGTGCAGCGGCTTCGGGAGAAGGAGCGGCAGTTGCTGC
CACAAGAGTGTCCAGTGGGCGCCAGGCCACCCTGCGGACAGTTTGC
CAGCGATGTCCAGTTTGTCTGAGGCGCACAGGGCCAGCCTAGCTG
GGAGGCCCTCTCAGACAGCTGTCCACCCCGGAACGCTGCCTAATT
CGTGCCAGCCTCCCTGTAAAGCCACGGGCTGCGCTGGGCTGTGAGCC
CCGAAAAACACTGACCCCGAGCCAGCCCCAGCCTCTCAGGCCCTG
GGCCTGCGGCCCTGTGACACCCACACCAGGCTGCTGCACAGACCTG
CGGGCCTGAATCAGGGTGCAGAGGAC

CLAIMS

1. The use of an isolated nucleic acid molecule comprising a sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 to detect or monitor cancer.

2. The use of a nucleic acid probe which is capable of hybridising under high stringency conditions to an isolated nucleic acid molecule comprising a sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56,

SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 to detect or monitor cancer.

3. A method of detecting or monitoring cancer comprising the step of detecting or monitoring elevated levels of a nucleic acid molecule comprising a sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 in a sample from a patient.

4. A method of detecting or monitoring cancer comprising the use of a nucleic acid molecule or probe according to claim 1 or claim 2 in combination with a reverse transcription polymerase chain reaction (RT-PCR).

5. A method of detecting or monitoring cancer comprising detecting or monitoring elevated levels of a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12,

SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66.

6. A method according to claim 5 comprising the use of an antibody selective for a protein or peptide as defined in claim 5 to detect the protein or peptide.

7. A method according to claim 7 comprising the use of an Enzyme-linked Immunosorbant Assay (ELISA).

18. Use or method according to any one of claims 1 to 7, wherein the cancer is prostate cancer is prostate cancer.

9. A kit for use with a method according to any one of claims 3-8 comprising a nucleic acid, protein or peptide, or an antibody as defined in any one of claims 3-8.

10. A method of prophylaxis or treatment of cancer comprising administering to a patient a pharmaceutically effective amount of nucleic acid molecule comprising a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5,

SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof.

11. A method of prophylaxis or treatment of cancer comprising administering to a patient a pharmaceutically effective amount of a nucleic acid molecule hybridisable under high stringency conditions to a nucleic acid molecule comprising a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof.

12. A method of prophylaxis or treatment of cancer comprising administering to a patient a pharmaceutically effective amount of a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof.

13. A method of prophylaxis or treatment of cancer comprising the step of administering to a patient a pharmaceutically effective amount of an antibody capable of specifically binding a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40,

SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66.

14. A method according to any one of claims 10 to 11, wherein the cancer is prostate cancer.

15. A vaccine comprising a nucleic acid molecule having a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof and a pharmaceutically acceptable carrier.

16. A vaccine comprising a protein or peptide comprising an amino acid sequence encoded by a nucleic acid sequence selected from SEQ.ID.1, SEQ.ID.2, SEQ.ID.3, SEQ.ID.4, SEQ.ID.5, SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11,

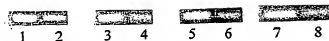
SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.31, SEQ.ID.32, SEQ.ID.33, SEQ.ID.34, SEQ.ID.35, SEQ.ID.36, SEQ.ID.37, SEQ.ID.38, SEQ.ID.39, SEQ.ID.40, SEQ.ID.41, SEQ.ID.42, SEQ.ID.43, SEQ.ID.44, SEQ.ID.45, SEQ.ID.46, SEQ.ID.47, SEQ.ID.48, SEQ.ID.49, SEQ.ID.50, SEQ.ID.51, SEQ.ID.52, SEQ.ID.53, SEQ.ID.54, SEQ.ID.55, SEQ.ID.56, SEQ.ID.57, SEQ.ID.58, SEQ.ID.59, SEQ.ID.60, SEQ.ID.61, SEQ.ID.62, SEQ.ID.63, SEQ.ID.64, SEQ.ID.65 and SEQ.ID.66 or a pharmaceutically effective fragment thereof, and a pharmaceutically acceptable carrier.

17. An isolated mammalian nucleic acid molecule comprising a nucleic acid sequence selected from SEQ.ID.6, SEQ.ID.7, SEQ.ID.8, SEQ.ID.9, SEQ.ID.10, SEQ.ID.11, SEQ.ID.12, SEQ.ID.13, SEQ.ID.14, SEQ.ID.15, SEQ.ID.16, SEQ.ID.17, SEQ.ID.18, SEQ.ID.19, SEQ.ID.20, SEQ.ID.21, SEQ.ID.22, SEQ.ID.23, SEQ.ID.24, SEQ.ID.25, SEQ.ID.26, SEQ.ID.27, SEQ.ID.28, SEQ.ID.29, SEQ.ID.30, SEQ.ID.43, SEQ.ID.44, SEQ.ID.52, SEQ.ID.60 and SEQ.ID.66 or a variant of a fragment thereof which encodes a prostate-associated antigen which is expressed in higher than normal concentrations in prostate cancer cells.

18. A vector comprising an isolated mammalian nucleic acid molecule according to claim 17.

19. A nucleic acid molecule comprising at least 15 nucleotides, the nucleic acid molecule being capable of hybridising to a molecule according to claim 17 under high stringency conditions.
20. An isolated protein or peptide comprising an amino acid sequence obtainable from a nucleic acid molecule according to claim 17, 18 or 19.
21. A nucleic acid probe capable of hybridising to a nucleic sequence as defined in SEQ ID 34, SEQ ID 35, SEQ ID 43, SEQ ID 44, SEQ ID 52, SEQ ID 60, SEQ ID 65 or SEQ ID 66, or a sequence complementary thereto, under high stringency conditions.

FIGURE 1



1. Esophageal cancer 2
2. Paired normal esophagus 2
3. Esophageal cancer 3
4. Paired normal esophagus 3
5. Esophageal cancer 4
6. Paired normal esophagus 4
7. Head and neck tumor 34
8. Paired normal head and neck 34

BEST AVAILABLE COPY